In Yeast Deletion Collection each gene is replaced by a KanMX cassette. This KanMX cassette is flanked by two 20bp barcodes specific for each knocked out gene (Up-tag and Down-tag). By sequencing these barcodes in a pool of the Yeast Deletion Collection, abundance of each mutant could be estimated. The

sequences of such flanking barcodes for each mutant is provided. (up-tag.fasta & down-tag.fasta). These barcodes were amplified with the primers U1 and p69 for Up-tag, and D2a and D1 for Down tag (See the schema below). The amplified cassettes were sequenced using 2x75nt reads.

In each of the fastq files, the sequence starts with one of the amplification primers (see below). Depending on the product being up or down-tag and depending on sequencing orientation, the mutant specific barcode is either on read1 or on read2 right after the amplification primer.

If the sequencing read starts with U1-primer, the barcode is at positions 19 to 38.

If the sequencing read starts with D1-primer, the barcode is at positions 18 to 37.

If the sequencing read starts with p69 or D2a, the barcode is on the paired read.

For matching the sequenced barcodes, 2 mismatches and 3 gaps were allowed.

Up-tag:

GATGTCCACGAGGTCTCTNNNNNNNNNNNNNNNNNNNCGTACGCTGCAGGTCGACGGATCCCCGGGTTAATT
AAGGCGCGCCAGATCTGTTTAGCTTGCCTCGTCCCCGCCGGGTCACCCGGCCAGCGACATGGAGGCCCAGAATAC
CCTCCTTGACAGTCTTGACGTGC

5'- U1_primer – 20bp of mutant_specific_Up_Barcode – 113bp of KanMX cassette – p69 primer – 3'

Down-tag:

TTTCGCCTCGACATCATCTGCCCAGATGCGAAGTTAAGTGCGCAGAAAGTAATATCATGCGTCAATCGTATGTGAA
TGCTGGTCGCTATACTGCTGTCGATTCGATACTAACGCCGCCATCCAGTGTCGAAAACGAGCTCGAATTCATCGAT
NNNNNNNNNNNNNNNNNNNCTACGAGACCGACACCG

5'- D2a_primer - 132bp of KanMX cassette – 20bp of mutant_specific_Dn_Barcode - D1 primer – 3'